

RAW SEQUENCE LISTING

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Application Serial Number: 09/993,292C
Source: IFW16
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RAW SEQUENCE LISTING

DATE: 07/15/2005

PATENT APPLICATION: US/09/993,292C

TIME: 10:04:59

Input Set : A:\09-993,292 Sequence Listing.txt

Output Set: N:\CRF4\07152005\I993292C.raw

3 <110> APPLICANT: University of Maryland, Baltimore
 4 GALEN, James E.
 6 <120> TITLE OF INVENTION: USE OF CLYA HEMOLYSIN FOR EXCRETION OF PROTEINS
 8 <130> FILE REFERENCE: A8461
 10 <140> CURRENT APPLICATION NUMBER: 09/993,292C
 11 <141> CURRENT FILING DATE: 2001-11-23
 13 <150> PRIOR APPLICATION NUMBER: US 60/252,516
 14 <151> PRIOR FILING DATE: 2000-11-22
 16 <160> NUMBER OF SEQ ID NOS: 25
 18 <170> SOFTWARE: PatentIn version 3.3
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 6271
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Artificial Sequence
 25 <220> FEATURE:
 26 <223> OTHER INFORMATION: pSEC84 Expression Plasmid
 28 <400> SEQUENCE: 1
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 31 gcgaggcata cggttggaaat aggggtaaac agacattcag aatgaatga cggtataaaa 120
 33 taaagttaat gatgatacg gtagttattc tagttgcag tgaagggttt gtttgacat 180
 35 tcagtgcgtg caaaatctta agaataagt attgattttt accttgaattt attattgctt 240
 37 gatgttaggt gcttatttcg ccattccgca ataatcttaa aaagttccct tgcatttaca 300
 39 tttgaaaca tctatacgca taaatgaaac atcttaaaag ttttagtatac atattcggt 360
 41 tggattattc tgcatttttggggagaatgg acttggcgac tgattatga gggtaatca 420
 43 gtagcagtgcataaaaaa gcaataaaag gcatataaca gatcgatctt aaacatccac 480
 45 aggaggatgg gatccaaaat aaggaggaaaa aaaaaatgac tagtattttt gcagaacaaa 540
 47 ctgtagaggt agttaaaaagc gcgatcgaaa ccgcagatgg ggcatttagat ctttataaca 600
 49 aataacctga ccaggtcatc ccctggaaaga cctttatgtaa aaccataaaa gaggtaagcc 660
 51 gttttaaaca ggagtactcg caggaagctt ctgttttagt tggtgatatt aaagtttgc 720
 53 ttatggacag ccaggacaag tattttgaag cgacacaaac tgtttatgaa tggtgtggtg 780
 55 tcgtgacgca attactctca gcttatattt tactatgttga tgaatataat gagaaaaaaag 840
 57 catcagccca gaaagacatt ctcatttaga tattatgttga tggtgtcaag aaactgaatg 900
 59 aagcgaaaa atctctctg acaagttcac aaagttcaa caacgcttcc gggaaactgc 960
 61 tggcatttgc tagccatttttactaatgatttttggaaaaa aagttagttat ttccagtac 1020
 63 aggtggatag aattcgtaag gaagctttagt ccgggtgtgc agccggcata gtcggcggtc 1080
 65 cgtttggatt aattatttcc tattcttatttgc gattgaaggaaatgttgc 1140
 67 cagaatttgcataacaggctaaaacgtc aaaatttctt tactatgttgc 1200
 69 tgaaacaagc gaataaaagat atcgatgcgg caaaatttgcattagccact gaaatagcag 1260
 71 caattgggaa gataaaaaacg gaaaccgaaa caaccagatttgc 1320
 73 taatgttttc ttattaaaaa ggagctgcaa agaaaatgttgc 1380
 75 aacaacgtca tggtaagaag acgttttcg aggttccgtca cgtcgctagc tgataaccta 1440
 77 gggccagcaa aaggccagga accgtaaaaa gggccgttgc 1500
 79 ccccccctt gacgagcatc acaaaaaatcg acgctcaagt cagagggtggc 1560

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83	gaccctgccg	cttaccggat	acctgtccgc	ctttctccct	tcgggaagcg	tggcgctttc	1680	
85	tcatagctca	cgctgttaggt	atctcagttc	ggtgttaggtc	ttcgctccca	agctgggctg	1740	
87	tgtgcacgaa	ccccccgttc	agcccgaccg	ctgcgcctta	tcccgtaact	atcgctttga	1800	
89	gtccaacccg	gtaagacacg	acttatacgcc	actggcagca	gccactggta	acagaggattag	1860	
91	cagagcggagg	tatgttaggctg	gtgctacaga	gttcttgaag	tggtggccctt	actacggctt	1920	
93	cactagaagg	acagtatttg	gtatctgcgc	tctgctgaag	ccagttaccc	tcggaaaaaag	1980	
95	agttggtagc	tcttgatccg	gcaaacaac	caccgctgg	agcgggtgg	ttttgtttt	2040	
97	caagcagcag	attacgcgc	aaaaaaaagg	atctcaagaa	gatcctttga	tctttctac	2100	
99	ggggctgtac	gctcagtaga	tctaaaacac	taggccaag	agtttgtaga	aacgaaaaaa	2160	
101	ggccatccgt	caggatggcc	ttctgcttaa	tttgcgttcc	ggcagttat	ggccggcg	2220	
103	ctgcccgc	ccctccgggc	cgttgc	caacgttcaa	atccgc	ttcc	2280	
105	tcctactca	gagagcgttc	accgacaaac	aacagataaa	acgaaaggcc	cagtcttgc	2340	
107	actgagcctt	tcgtttatt	tgatgcctgg	cagtccctta	ctctcgcatg	gggagacccc	2400	
109	acactaccat	cggcgttacg	gcgtttca	tctgagttcg	gcatggg	tc aggtggacc	2460	
111	accgcgtac	tgccgc	cagg	caaattctgt	tttac	tcagac	2520	
113	atctgtatca	ggctgaaaat	cttctctcat	ccgcca	aaac	agccaagctg	2580	
115	atcgctgaat	attcctttt	gttccgacca	tcaggc	acct	gagtcgtgt	2640	
117	acattcagtt	cgctgcgtc	acggctctgg	cagtaatgg	gggt	aaatgg	2700	
119	gcctttat	gattcatgca	aggaaactac	ccataataca	agaaa	agcccc	2760	
121	tctcagg	ggc	tttatggc	ggtctgtat	gtgg	tgctat	2820	
123	agttcctg	cc	ctgtat	ttt	ccat	gacttcgt	2880	
125	agactggct	atgcaccc	cac	taaggc	gacg	gtatcatcaa	2940	
127	tcaaccggat	ctaaa	acact	agccc	aaact	ttc	atcataag	3000
129	tcgtgtat	ggc	agg	ttggc	gtc	tttgc	3060	
131	aagaactcg	caagaagg	cg	atagaagg	cg	atgcgtgc	3120	
133	taaagcac	gga	aggc	ggc	tttgc	ccat	atcacgg	3180
135	gccaacg	tgt	cctgata	gcgg	tcc	ccgc	atcc	3240
137	aaaaagc	ggc	catttcc	cat	gat	atcc	tcac	3300
139	agatc	cgt	cg	ggc	gtt	ccat	ggc	3360
141	ccctgat	gtt	cgt	cc	atc	atc	tcgt	3420
143	gtc	gt	gtt	cg	tt	tcg	atc	3480
145	tgc	ag	cc	gtc	at	ttt	tcgt	3540
147	gac	agg	ga	cgt	ttt	tcgt	ccat	3600
149	aca	ac	gt	tc	ttt	tcgt	ccat	3660
151	gc	ct	gt	cc	at	tc	tcgt	3720
153	cgc	cc	tc	gt	ttt	tcgt	ccat	3780
155	cag	tc	at	gc	ttt	tcgt	ccat	3840
157	tgt	ca	at	tc	ttt	tcgt	ccat	3900
159	cat	ca	gg	cc	at	tc	tcgt	3960
161	cc	ag	gg	cc	ttt	tcgt	ccat	4020
163	gggg	ctt	ac	cc	ttt	tcgt	ccat	4080
165	at	cc	ttt	cc	ttt	tcgt	ccat	4140
167	at	gaa	agg	cc	ttt	tcgt	ccat	4200
169	gtc	ca	at	at	tc	tcgt	ccat	4260
171	ctt	cg	gtt	cc	ttt	tcgt	ccat	4320
173	at	gt	gg	ac	ttt	tcgt	ccat	4380
175	tat	ttt	ctg	cc	ttt	tcgt	ccat	4440
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179	gaaaataatc	cgctcattca	gaccgttac	ggaaatccg	tgtgattgtt	gccgcata	cac	4560	
181	gctgcctccc	ggagttgtc	tcgagcac	ttgttacccg	ccaaacaaaa	cccaaaaaca		4620	
183	accat	accatacc	aaccaataa	aacacaaaaa	caagacaat	aatcattgat	tgatggttga	4680	
185	aatgggtaa	acttgacaaa	caaaccact	taaaacccaa	aacataccca	aacacacacc		4740	
187	aaaaaaacac	cataaggagt	tttataatg	ttggattca	ttgatgacgg	ttcaacaaac		4800	
189	atcaaactac	agtggcagga	aagcagcga	acaattaaac	agcacat	ccgaacagc		4860	
191	ttcaaacgcg	agtggcagt	ctcttttgt	gataaaaagg	tctttaacta	cacactgaac		4920	
193	ggcgaacagt	attcattga	tccaaatcagc	ccggatgctg	tagtcaca	caatatcgca		4980	
195	tggcaataca	g	gcgacgtta	tgtcgttgca	gtgcatc	ccttactgac	cagtggctg	5040	
197	ccggtaagcg	aagtgat	atgttgac	ttttgcaca	cttcctctga	cagagtatta	cgacagaaat	5100	
199	aaccaaccca	atacgaaaaa	tattgagcgt	aagaaagcaa	acttccggaa	aaaaattaca		5160	
201	ttaaatggcg	gggatacatt	cacaataaaa	gatgtaaaag	tcatgcctga	atctataccg		5220	
203	gcaggttat	g	agttctaca	agaactggat	gagttagatt	ctttattaat	tatagatctc	5280	
205	gggggcacca	cattagat	ttctcaggt	atggggaaat	tatcggggat	cagaaaata		5340	
207	tacggagact	catcttgg	tgtctctcg	gttacatctg	cagtaaaaga	tgcccttct		5400	
209	cttgcgagaa	caaaaggaag	tagctatctt	gctgacgata	taatcatca	cagaaaagat		5460	
211	aataactatc	tgaagcaac	aattaatgt	gagaacaaaa	tatcaatagt	caccgaagca		5520	
213	atgaatgaag	cacttcgtaa	acttgagcaa	cgtgtattaa	atacgctaa	tgaat	ttct	5580	
215	ggttatactc	atgttat	gtgtgtt	ttataggcgt	ggcgcagaat	taatatgcga	tgcagtaaaa	5640	
217	aaacacacac	agattcgt	gtaacgttt	ttcaaaacca	ataactctca	atatgattta		5700	
219	gttaacggt	tgat	atctcat	aggtat	ttatggacaa	g	gcgcagaacc	attgccttca	5760
221	aactaaatcc	agatgt	aaat	tttgcgtt	tgat	actg	gacagtatcc		5820
223	cgcaagggga	acgaagccgc	cttaaccggg	ccgca	ctgac	ggcagg	gtct	gccttata	5880
225	gacaagatcc	ccggacccct	ttcctttat	gtgagctg	ct	gacgaa	agaa	accacat	5940
227	cagatatcg	gaatatatt	tgatcgctat	ttccaa	aga	gatggcc	gtt	attctt	6000
229	caatagt	cac	tcacaa	caag	agcaaaa	tgat	gaagag	acc	6060
231	atgcgatgaa	gctaataat	taattcaatt	attattg	gtgt	tccctt	tatc	cactatcagg	6120
233	ctggataaa	ggaactca	taagttattt	tcttacc	gt	cattacataa	tcgtt	tattat	6180
235	gaaataatcg	tttgcactgt	ctctgttatt	cagg	caattt	caataa	aggc	acttgctcac	6240
237	gtctgtcat	tttctgaa	ac	tcttcat	gt	g			6271

240 <210> SEQ ID NO: 2

241 <211> LENGTH: 305

242 <212> TYPE: PRT

243 <213> ORGANISM: *Salmonella typhi*

245 <400> SEQUENCE: 2

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248	1				5				10					15		
251	Ile	Glu	Thr	Ala	Asp	Gly	Ala	Leu	Asp	Leu	Tyr	Asn	Lys	Tyr	Leu	Asp
252					20				25					30		
255	Gin	Val	Ile	Pro	Trp	Lys	Thr	Phe	Asp	Glu	Thr	Ile	Lys	Glu	Leu	Ser
256					35				40					45		
259	Arg	Phe	Lys	Gln	Glu	Tyr	Ser	Gln	Glu	Ala	Ser	Val	Leu	Val	Gly	Asp
260					50				55					60		
263	Ile	Lys	Val	Leu	Leu	Met	Asp	Ser	Gln	Asp	Lys	Tyr	Phe	Glu	Ala	Thr
264					65				70			75		80		
267	Gln	Thr	Val	Tyr	Glu	Trp	Cys	Gly	Val	Val	Thr	Gln	Leu	Leu	Ser	Ala
268									85			90		95		
271	Tyr	Ile	Leu	Leu	Phe	Asp	Glu	Tyr	Asn	Glu	Lys	Lys	Ala	Ser	Ala	Gln
272									100			105		110		

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275 Lys Asp Ile Leu Ile Arg Ile Leu Asp Asp Gly Val Lys Lys Leu Asn
 276 115 120 125
 279 Glu Ala Gln Lys Ser Leu Leu Thr Ser Ser Gln Ser Phe Asn Asn Ala
 280 130 135 140
 283 Ser Gly Lys Leu Leu Ala Leu Asp Ser Gln Leu Thr Asn Asp Phe Ser
 284 145 150 155 160
 287 Glu Lys Ser Ser Tyr Phe Gln Ser Gln Val Asp Arg Ile Arg Lys Glu
 288 165 170 175
 291 Ala Tyr Ala Gly Ala Ala Gly Ile Val Ala Gly Pro Phe Gly Leu
 292 180 185 190
 295 Ile Ile Ser Tyr Ser Ile Ala Ala Gly Val Ile Glu Gly Lys Leu Ile
 296 195 200 205
 299 Pro Glu Leu Asn Asn Arg Leu Lys Thr Val Gln Asn Phe Phe Thr Ser
 300 210 215 220
 303 Leu Ser Ala Thr Val Lys Gln Ala Asn Lys Asp Ile Asp Ala Ala Lys
 304 225 230 235 240
 307 Leu Lys Leu Ala Thr Glu Ile Ala Ala Ile Gly Glu Ile Lys Thr Glu
 308 245 250 255
 311 Thr Glu Thr Thr Arg Phe Tyr Val Asp Tyr Asp Asp Leu Met Leu Ser
 312 260 265 270
 315 Leu Leu Lys Gly Ala Ala Lys Lys Met Ile Asn Thr Cys Asn Glu Tyr
 316 275 280 285
 319 Gln Gln Arg His Gly Lys Lys Thr Leu Phe Glu Val Pro Asp Val Ala
 320 290 295 300
 323 Ser
 324 305
 327 <210> SEQ ID NO: 3
 328 <211> LENGTH: 102
 329 <212> TYPE: DNA
 330 <213> ORGANISM: Artificial Sequence
 332 <220> FEATURE:
 333 <223> OTHER INFORMATION: Cloning Primer
 335 <400> SEQUENCE: 3
 336 ggatccaaaa taaggaggaa aaaaaatga ctagtattt tgcagaacaa actgttagagg 60
 338 tagttaaaag cgcgatcgaa accgcagatg gggcattaga tc 102
 341 <210> SEQ ID NO: 4
 342 <211> LENGTH: 101
 343 <212> TYPE: DNA
 344 <213> ORGANISM: Artificial Sequence
 346 <220> FEATURE:
 347 <223> OTHER INFORMATION: Cloning Primer
 349 <400> SEQUENCE: 4
 350 cctaggttat cagctacgca cgtcaggaac ctcgaaaagc gtcttcttac catgacgttg 60
 352 ttggtattca ttacaggtgt taatcatttt ctttgcagct c 101
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 356 <211> LENGTH: 97
 357 <212> TYPE: DNA
 358 <213> ORGANISM: Artificial Sequence
 360 <220> FEATURE:

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361 <223> OTHER INFORMATION: Cloning Primer
 363 <400> SEQUENCE: 5
 364 cacggtaaga agacgcttt cgaggttccct gacgtcgcta gctgataacc taggtcatgt 60
 366 tagacagctt atcatcgata agctttaatg cggtatg 97
 369 <210> SEQ ID NO: 6
 370 <211> LENGTH: 69
 371 <212> TYPE: DNA
 372 <213> ORGANISM: Artificial Sequence
 374 <220> FEATURE:
 375 <223> OTHER INFORMATION: Cloning Primer
 377 <400> SEQUENCE: 6
 378 agatctacta gtgtcgacgc tagctatcag gtcgaggtgg cccggctcca tgcaccgcga 60
 380 cgcAACGCG 69
 383 <210> SEQ ID NO: 7
 384 <211> LENGTH: 60
 385 <212> TYPE: DNA
 386 <213> ORGANISM: Artificial Sequence
 388 <220> FEATURE:
 389 <223> OTHER INFORMATION: Cloning Primer
 391 <400> SEQUENCE: 7
 392 actagtaccc cagaaacgct ggtgaaagta aaagatgctg aagatcagtt gggtgacacga 60
 395 <210> SEQ ID NO: 8
 396 <211> LENGTH: 101
 397 <212> TYPE: DNA
 398 <213> ORGANISM: Artificial Sequence
 400 <220> FEATURE:
 401 <223> OTHER INFORMATION: Cloning Primer
 403 <400> SEQUENCE: 8
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 406 ttaatcagtg aggcacctat ctcagcgatc tgtctatttc g 101
 409 <210> SEQ ID NO: 9
 410 <211> LENGTH: 101
 411 <212> TYPE: DNA
 412 <213> ORGANISM: Artificial Sequence
 414 <220> FEATURE:
 415 <223> OTHER INFORMATION: Cloning Primer
 417 <400> SEQUENCE: 9
 418 cggaaatagac agatcgctga gataggtgcc tcactgatta agcattggta atgacctagg 60
 420 ctagctcatg tttgacagct tatcatcgat aacctttaat g 101
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 424 <211> LENGTH: 71
 425 <212> TYPE: DNA
 426 <213> ORGANISM: Artificial Sequence
 428 <220> FEATURE:
 429 <223> OTHER INFORMATION: Cloning Primer
 431 <400> SEQUENCE: 10
 432 gcgcaactgtt aaagaaacgta accaaaagcc atataaggaa acatacgca tttccatat 60
 434 tacacgccccat g 71
 437 <210> SEQ ID NO: 11

VERIFICATION SUMMARY

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